

RAW SEQUENCE LISTING

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Application Serial Number: 10/523,479
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DATE: 01/26/2006

PATENT APPLICATION: US/10/523,479

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3 <110> APPLICANT: MORAN, MAGDALENE M.
 4 CHONG, JAYHONG A.
 5 RAMSEY, IAN SCOTT
 6 CLAPHAM, DAVID E.
 8 <120> TITLE OF INVENTION: SPERM-SPECIFIC CATION CHANNEL, CATSPER-3, AND

USES

9 THEREFOR
 11 <130> FILE REFERENCE: 110313.138US2
 13 <140> CURRENT APPLICATION NUMBER: 10/523,479
 14 <141> CURRENT FILING DATE: 2005-02-04
 16 <150> PRIOR APPLICATION NUMBER: PCT/US03/24432
 17 <151> PRIOR FILING DATE: 2003-08-04
 19 <150> PRIOR APPLICATION NUMBER: 60/401,863
 20 <151> PRIOR FILING DATE: 2002-08-07
 22 <160> NUMBER OF SEQ ID NOS: 7
 24 <170> SOFTWARE: PatentIn Ver. 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1203
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
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 34 cgccccctct ccctgcagag taccattcac gagtcctacg gtcggccaga ggagcaagtg 180
 35 ctcatcaacc gccaggaaat cacgaacaaa gcggacgcct gggacatgca ggagtcatc 240
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 38 cactatgagt tggtctctac catagatgac attgtgctga ccaccttct ttgtgaggtt 420
 39 ctcccttggt ggctcaatgg cttctggatt ttctggaagg acggctggaa catcctcaac 480
 40 ttcaattatc tctttatctt gctcttgccg ttcttcatta atgaaatcaa tattccctcc 540
 41 atcaactaca ctctcagggc gcttcgtctg gtgcatgtgt gcatggcggg ggagccctc 600
 42 gcccggatca tccgcgtcat cctgcagtcg gtgcctgaca tggccaatat catggtcctc 660
 43 atcctcttct tcatgctggt tttttccgtg tttggagtaa cactctttgg tgcattcgtg 720
 44 cccaagcatt tccagaacat acaggttgcg ctgtacaccc tcttcatctg catcacccag 780
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 46 attgggggtg ccatctactt taccatcttc atcaccatcg gtgccttcat tggcatcaac 900
 47 ctgttcgtca tcgtggtgac caccaacctg gagcaaatga tgaaggcagg agagcaggga 960
 48 caacagcaac gaataacctt tagtgagaca ggcgcagagg aagaggagga gaatgaccag 1020
 49 ctgccactgg tgcatttgtt ggtcgccgcg tcggagaaat ctggtctcct ccaggaaacc 1080
 50 cttgcgggag gccccctgtc gaacctctca gaaaacacgt gtgacaactt ttgcttggtg 1140
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 52 tag 1203
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 400

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64 Gly Leu Glu Gly Trp Gly Gly Thr Gln Glu Asp Arg Met Gly Phe Gly
65 20 25 30
67 Gly Ala Val Ala Ala Leu Arg Gly Arg Pro Ser Pro Leu Gln Ser Thr
68 35 40 45
70 Ile His Glu Ser Tyr Gly Arg Pro Glu Glu Gln Val Leu Ile Asn Arg
71 50 55 60
73 Gln Glu Ile Thr Asn Lys Ala Asp Ala Trp Asp Met Gln Glu Phe Ile
74 65 70 75 80
76 Thr His Met Tyr Ile Lys Gln Leu Leu Arg His Pro Ala Phe Gln Leu
77 85 90 95
79 Leu Leu Ala Leu Leu Leu Val Ile Asn Ala Ile Thr Ile Ala Leu Arg
80 100 105 110
82 Thr Asn Ser Tyr Leu Asp Gln Lys His Tyr Glu Leu Phe Ser Thr Ile
83 115 120 125
85 Asp Asp Ile Val Leu Thr Ile Leu Leu Cys Glu Val Leu Leu Gly Trp
86 130 135 140
88 Leu Asn Gly Phe Trp Ile Phe Trp Lys Asp Gly Trp Asn Ile Leu Asn
89 145 150 155 160
91 Phe Ile Ile Val Phe Ile Leu Leu Leu Arg Phe Phe Ile Asn Glu Ile
92 165 170 175
94 Asn Ile Pro Ser Ile Asn Tyr Thr Leu Arg Ala Leu Arg Leu Val His
95 180 185 190
97 Val Cys Met Ala Val Glu Pro Leu Ala Arg Ile Ile Arg Val Ile Leu
98 195 200 205
100 Gln Ser Val Pro Asp Met Ala Asn Ile Met Val Leu Ile Leu Phe Phe
101 210 215 220
103 Met Leu Val Phe Ser Val Phe Gly Val Thr Leu Phe Gly Ala Phe Val
104 225 230 235 240
106 Pro Lys His Phe Gln Asn Ile Gln Val Ala Leu Tyr Thr Leu Phe Ile
107 245 250 255
109 Cys Ile Thr Gln Asp Gly Trp Val Asp Ile Tyr Ser Asp Phe Gln Thr
110 260 265 270
112 Glu Lys Arg Glu Tyr Ala Met Glu Ile Gly Gly Ala Ile Tyr Phe Thr
113 275 280 285
115 Ile Phe Ile Thr Ile Gly Ala Phe Ile Gly Ile Asn Leu Phe Val Ile
116 290 295 300
118 Val Val Thr Thr Asn Leu Glu Gln Met Met Lys Ala Gly Glu Gln Gly
119 305 310 315 320
121 Gln Gln Gln Arg Ile Thr Phe Ser Glu Thr Gly Ala Glu Glu Glu Glu
122 325 330 335
124 Glu Asn Asp Gln Leu Pro Leu Val His Cys Val Val Ala Arg Ser Glu
125 340 345 350
127 Lys Ser Gly Leu Leu Gln Glu Pro Leu Ala Gly Gly Pro Leu Ser Asn
128 355 360 365

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130 Leu Ser Glu Asn Thr Cys Asp Asn Phe Cys Leu Val Leu Glu Ala Ile
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133 Gln Glu Asn Leu Arg Gln Tyr Lys Glu Ile Arg Asp Glu Leu Asn Met
134 385      390      395      400
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141 <211> LENGTH: 1329
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145 <400> SEQUENCE: 3
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148 agagatgtca tggagaagaa ggatgcctgg gatgtacagg aattcatcac tcaaattgat 180
149 atcaagcagt tgctccgcca tccggccttc cagctgctgc tggcctttct gctgctgtcc 240
150 aacgccatca ccattgccct tcgcaccaac tcttatctcg gtcagaaaca ctacgagcta 300
151 ttctcgacca tagatgacat tgtgttgacg atccttatct gcgaggttct gcttggttgg 360
152 cttaacggct tctggatttt ctggaaggat ggctggaata tcctcaactt cgcaattgtc 420
153 tttatcttgt ttatgggggt cttcataaaa caacttgaca tggttgccat cacctaccct 480
154 ctcagggtgc tccggctggg gcatgtgtgt atggcggtgg aaccctggc cagaatcatc 540
155 aaggttatcc tgcagtcgat gccagacttg gccaatgtca tggctctcat cctcttcttc 600
156 atgctggtat tctctgtgtt tggggtcacg ctcttcggtg catttggtgc caagcatttc 660
157 cagaacatgg gggttgccct gtacacgctc ttcacttgca tcaactcagg tggatggctg 720
158 gacatctaca ctgacttcca gatggatgaa agagagtacg cgatggaggt cgggggcgcc 780
159 atctactttg ccgctctttat caccctcggg gccttcattg gtctcaactt gttcgtcgtc 840
160 gtggtgacca caaacctgga acaaatgatg aagaccggcg aggaagaggg acacctgaac 900
161 ataaagttta ctgagacaga agaggatgag gactggaccg acgagctgcc actggtgcat 960
162 tgtacagagg cccgcaagga tacttccact gtccccaagg aaccactggt tgggggcccc 1020
163 ctgagtaacc tcacagaaaa gacctgcgat aacttctgct tggtgcttga agcaatacag 1080
164 gagaacttga tggagtacaa agagatccga gaggaactca acatgatcgt ggaggaagtg 1140
165 tcctccatcc ggttcaacca ggagcagcaa aatgtgatcc tacacaagta tacctccaaa 1200
166 agcgccacct tcctaagcga gccccagaa ggggctaaca agcaagactt gatcactgcg 1260
167 ctggctcagca gggaaaagggt gtctgattct aacataaaca tggttaacaa acacaagttc 1320
168 agccactga
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172 <211> LENGTH: 442
173 <212> TYPE: PRT
174 <213> ORGANISM: Mus sp.
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181      20      25      30
183 Glu Glu Gln Val Leu Ile Asn Arg Arg Asp Val Met Glu Lys Lys Asp
184      35      40      45
186 Ala Trp Asp Val Gln Glu Phe Ile Thr Gln Met Tyr Ile Lys Gln Leu
187      50      55      60
189 Leu Arg His Pro Ala Phe Gln Leu Leu Leu Ala Phe Leu Leu Leu Ser
190 65      70      75      80
192 Asn Ala Ile Thr Ile Ala Leu Arg Thr Asn Ser Tyr Leu Gly Gln Lys
193      85      90      95

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195 His Tyr Glu Leu Phe Ser Thr Ile Asp Asp Ile Val Leu Thr Ile Leu
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198 Ile Cys Glu Val Leu Leu Gly Trp Leu Asn Gly Phe Trp Ile Phe Trp
199          115          120          125
201 Lys Asp Gly Trp Asn Ile Leu Asn Phe Ala Ile Val Phe Ile Leu Phe
202          130          135          140
204 Met Gly Phe Phe Ile Lys Gln Leu Asp Met Val Ala Ile Thr Tyr Pro
205 145          150          155          160
207 Leu Arg Val Leu Arg Leu Val His Val Cys Met Ala Val Glu Pro Leu
208          165          170          175
210 Ala Arg Ile Ile Lys Val Ile Leu Gln Ser Met Pro Asp Leu Ala Asn
211          180          185          190
213 Val Met Ala Leu Ile Leu Phe Phe Met Leu Val Phe Ser Val Phe Gly
214          195          200          205
216 Val Thr Leu Phe Gly Ala Phe Val Pro Lys His Phe Gln Asn Met Gly
217          210          215          220
219 Val Ala Leu Tyr Thr Leu Phe Ile Cys Ile Thr Gln Asp Gly Trp Leu
220 225          230          235          240
222 Asp Ile Tyr Thr Asp Phe Gln Met Asp Glu Arg Glu Tyr Ala Met Glu
223          245          250          255
225 Val Gly Gly Ala Ile Tyr Phe Ala Val Phe Ile Thr Leu Gly Ala Phe
226          260          265          270
228 Ile Gly Leu Asn Leu Phe Val Val Val Val Thr Thr Asn Leu Glu Gln
229          275          280          285
231 Met Met Lys Thr Gly Glu Glu Glu Gly His Leu Asn Ile Lys Phe Thr
232          290          295          300
234 Glu Thr Glu Glu Asp Glu Asp Trp Thr Asp Glu Leu Pro Leu Val His
235 305          310          315          320
237 Cys Thr Glu Ala Arg Lys Asp Thr Ser Thr Val Pro Lys Glu Pro Leu
238          325          330          335
240 Val Gly Gly Pro Leu Ser Asn Leu Thr Glu Lys Thr Cys Asp Asn Phe
241          340          345          350
243 Cys Leu Val Leu Glu Ala Ile Gln Glu Asn Leu Met Glu Tyr Lys Glu
244          355          360          365
246 Ile Arg Glu Glu Leu Asn Met Ile Val Glu Glu Val Ser Ser Ile Arg
247          370          375          380
249 Phe Asn Gln Glu Gln Gln Asn Val Ile Leu His Lys Tyr Thr Ser Lys
250 385          390          395          400
252 Ser Ala Thr Phe Leu Ser Glu Pro Pro Glu Gly Ala Asn Lys Gln Asp
253          405          410          415
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256          420          425          430
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259          435          440
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263 <211> LENGTH: 2079
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 5

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270 agacacatca cctgcagcca cccccacaca gcgcagccca cggacctcct ttggctctct 180
271 gacaggtgct gggctggagt tgggagctgg gctgggggct ggggtgggca catcctcatc 240
272 ctgctcttcc ctcccacaga cagcagtga gaggcactgg aaggaatggt acgggggctg 300
273 aggcagggtg gcgtgtccct cctaggccag ccacagcccc tgaccagga acagtggcgg 360
274 agctctttca tgcggcgcaa ccgagacct cagctcaatg agcgagtga ccgtgtgcgg 420
275 gcgctacaga gcacactcaa ggtcagctgg ggggctctgg gcacagcaag ggactaggct 480
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277 ccagactcag ctccggacct tgggcttagc agctgacagc gggctcagct gtggactggg 600
278 ccaggctctg ggttccgagt ggggatttga gtctcaccta ggctcctcg gccacgctgg 660
279 ccagggtgctg gcttccaggc accggacctc cggagtgaag tctggcctcg ggctctgccc 720
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301 ttctctccag gttggaattc ctcagtagaa tgcagacggc tggaggtcac agaggcctct 2040
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316 <212> TYPE: DNA

317 <213> ORGANISM: Homo sapiens

319 <400> SEQUENCE: 7

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